CRFE

ACCESS DB # *153572*

PLEASE PRINT CLEARLY

Scientific and Technical Information Center
SEARCH REQUEST FORM

Requester's Full Name: *TERRA GIBBS*   Examiner # : *79523* Date: *5/16/05*

Art Unit: *1635*   Phone Number: *2-0758*   Serial Number: *10/005,337*

Location (Bldg/Room#): *2D10* (Mailbox #): *2C18*   Results Format Preferred (circle): **PAPER** DISK

Remsen

ME

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Date: _____

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

I am not sure if this can be done...

Attached as Exhibit B is a nucleotide sequence ~250 bp in length.

Applicant's have provided this BLAST search with a result of   see Query 1.
   ^comparison

completed
5-25-05
Barb O'Bryen
22518

83% identity.

1.   I need the same comparison with an result of 90% identity
    with SEQ ID No: 2 (nucleobases 1715-2060) as Exhibit B shows
        ↓ USSN 10/005,337

2.   I also need the same comparison with a result of 93% identity
    with SEQ ID No: 1 *NA-2358* — 0 this is confusing)

5-25-05

Terra,

Seq 1 has 100% local similarity with "Query 1".
Seq1 is much longer than Query1, so the overall query match is low & can't be improved significantly.

I tried 8 different sets of parameter changes (altering Gap penalty &/or Gap size penalty) to get the best match between Seq 2, nt 1715 - 3060 vs Query 1. The best I could come up with was 82.5%. Best Local Similarity (green tab).

Please let me know if you have questions.

Barb

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                           (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       May 25, 2005, 16:32:23 ; Search time 0.001 Seconds
                                        (without alignments)
                                        1589.292 Million cell updates/sec

Title:        US-10-005-337A-1-COPY
Perfect score: 2358
Sequence:     1 ggatcccttcatgttaaca.........caggtcggaggccaccatgg 2358

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 0.5
Searched:     1 seqs, 337 residues

Total number of hits satisfying chosen parameters:     2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    new.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                          SUMMARIES
                 %
                 Query
Result           Match
No.   Score      Length  DB Length  ID              Description
---   -----      ------  -- ------  --              -----------
  1    337       14.3    337   1    QUERY_1         Entered [bobryen
c 2     17.4      0.7    337   1    QUERY_1         Entered [bobryen

                          ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match            14.3%;   Score 337; DB 1; Length 337;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1972 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCCGATACGTGGGATGACTCGCATTGCTG 2031
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCCGATACGTGGGATGACTCGCATTGCTG 60

Qy 2032 AGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGGCATACGC 2091
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGGCATACGC 120

Qy 2092 CGCGGCCAGCTTGTCATCTCCCTCTTGGGCTTCCAGACACTAAGTCTGGAATGAAAATT 2151
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CGCGGCCAGCTTGTCATCTCCCTCTTGGGCTTCCAGACACTAAGTCTGGAATGAAAATT 180

Qy 2152 CACCTGCCTCTGAATTGGCCACTGGTGGGGACAGGGGGTGTGACTTGGCTTCCCAGGCTGG 2211
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CACCTGCCTCTGAATTGGCCACTGGTGGGGACAGGGGGTGTGACTTGGCTTCCCAGGCTGG 240

Qy 2212 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGGCTCCACAGGGC 2271


Db  241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGGCTCCACAGGGC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 2272 CAGTTCCAGGGGTCATCCACCAAGAGAAAAACATA 2308
        |||||||||||||||||||||||||||||||||||
Db  301 CAGTTCCAGGGGTTCATCCACCAAGAGAGAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match            0.7%;   Score 17.4;   DB 1; Length 337;
Best Local Similarity 53.7%;   Pred. No. 0;
Matches 36; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1709 CAGGGCCATTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGG 1768
        ||||  ||||| |  ||||  ||||   |||||| ||    |||  ||||| |||||||
Db  186 CAGGTGAATTTCATTCCAGACTTAGTGTCTGGGAAGCCCAAGAGAGGGAGGATGACAAGCTG 127

Qy 1769 CACCCAG 1775
        |||  ||
Db  126 GCCGCGG 120

Search completed: May 25, 2005, 16:32:23
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on:       May 25, 2005, 16:32:23 ; Search time 0.001 Seconds
                                        (without alignments)
                                        233.204 Million cell updates/sec

Title:        US-10-005-337A-2_1715-2060
Perfect score: 346
Sequence:     1 gcaatgtcaacagacagctg.........cgacagaaaacatcaaga 346

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 0.5
Searched:     1 seqs, 337 residues

Total number of hits satisfying chosen parameters:     2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    new.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                          SUMMARIES
                 %
                 Query
Result           Match
No.   Score      Length  DB Length  ID              Description
---   -----      ------  -- ------  --              -----------
  1   198.2      57.3    337   1    QUERY_1         Entered [bobryen
c 2    12.8       3.7    337   1    QUERY_1         Entered [bobryen

                          ALIGNMENTS
```

```
RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match        57.3%;    Score 198.2;   DB 1;  Length 337;
Best Local Similarity   80.8%;    Pred. No. 0;
Matches  277;  Conservative    0;  Mismatches   58;  Indels    8;  Gaps    4;

Qy      1 GCAATGTCAACAGACAGCTGTCCCCTGAC-TCTTGACAAATAGGATGACTTGCATTGCTG  59
          ||||| ||||||| ||||||||||||||||| || || |   |  |  | ||||||||||
Db      1 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCCGATACGTGGGATGACTCGCATTGCTG  60

Qy     60 AGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACATTCTTCCTGATTCACATATTC  119
          |||||||| ||| |||| ||| |||||||||||||||||||||| ||||
Db     61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGCCATACGC  120

Qy    120 AGCAGGGTTAGCTTGCTGTCCTCCCCTCCCTTCAGCTTCCCAGACACTGAGTCTGGAATGA  179
          ||| |     |  |||||  ||||||||||| ||||||||||||||||||||||||
Db    121 CGCCG-----CCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGA  175

Qy    180 AAATTCACCTGCCTCTGAGTTGGGCTCCTAATGGGGGCGGGAGTGTTACTTCGGTTCCCAG  239
          |||||||||||||||||||||||||| | |||| ||  | |  ||| || | |||||||||
Db    176 AAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTCCCAG  235

Qy    240 GTTCGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCCGTGTGGAGGGCCCCAG  299
          | |||||||||||||||||| |||||| | |   |  |  ||  ||||||||||||
Db    236 GCTCGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTCGTGTGTGGAGGGGCTCCA  294

Qy    300 CAGGGCCAACTCCAGGGATTCCTTC-CACGACAGAAAAACATA  341
          |||| ||    ||||||||||||||| |||||||||||||||
Db    295 CAGGGCCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATA  337
```

```
RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match         3.7%;    Score 12.8;    DB 1;  Length 337;
Best Local Similarity   51.8%;    Pred. No. 0;
Matches   29;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy     85 TGGCCCTCTCACATTTCTTCCTGATTCACATATTCACATATTCAGCAGGGTTAGCTTGTCCTTCC  140
          ||| |||  ||  | || |  |   |||    | || ||    || || || || | ||
Db    294 TGGAGCCCCCTCCACACCAGCCCGTTATATAGCTTAGGGCTCGGTGAGATAAATCTTCC  239
```

Search completed: May 25, 2005, 16:32:24
Job time : 1 secs

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         GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    May 25, 2005, 16:34:51 ; Search time 0.872041 Seconds
                              (without alignments)
                              1.822 Million cell updates/sec

Title:          US-10-005-337A-1-COPY
Perfect score:  2358
Sequence:       1 ggatccttcatgttaaca.........caggtcggaggccacatgg 2358

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 0.0

Searched:       1 seqs, 337 residues

Total number of hits satisfying chosen parameters:   2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  new.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                            SUMMARIES

                           %
Result         Query
 No.    Score  Match Length DB  ID        Description
------  -----  ----- ------ --  --------  -----------
   1     337   14.3    337  1   QUERY_1   Entered [bobryen
c  2     21.4   0.9    337  1   QUERY_1   Entered [bobryen

                            ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match    14.3%;  Score 337;  DB 1;  Length 337;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches  337;  Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy 1972 GCAATATAACAGGCAGCTGTCCCCTGCTTCCGATACGTGGGATGACTCGGATTGCTG 2031
        |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GCAATATTAACAGGCAGCTGTCCCCTGCTTCCCGATACGTGGGATGACTCGCATTGCTG 60

Qy 2032 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTTCTTCCTGATTCGCATACGC 2091
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTTCTTCCTGATTCGCATACGC 120

Qy 2092 CGCGGGCCAGCTTGTCATCTCCCTCTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 2151
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CGCGGCCAGCTTGTCATCTCCCTCTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 180

Qy 2152 CACCTGCCTCTGAATTGGCCACTGGTGGGGCACGAGGGGTGTGACTTGGCTTCCCAGGCTGG 2211
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CACCTGCCTCTGAATTGGCCACTGGTGGGGCACGAGGGGTGTGACTTGGCTTCCCAGGCTGG 240

Qy 2212 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGGCTCGGTGTGGAGGGGCTCCACAGGGC 2271
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGGCTGGTGTGGAGGGGCTCCACAGGGC 300

Qy 2272 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 2308
        |||||||||||||||||||||||||||||||||||
Db  301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 337


RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match     0.9%;  Score 21.4;  DB 1;  Length 337;
Best Local Similarity  10.8%;  Pred. No. 0;
Matches  162;  Conservative  0; Mismatches  151; Indels 1186; Gaps  5;

Qy  551 TCTTATGGGTGGAGCCAAGACGCATCGTGGGTGAGCGAAGACGCAACCTCACCTTCTAG 610
        ||||| ||  | | ||||  || | || ||
Db  325 TCTTGTGGATGAACCCCTGGAACTGGCCCGTGGAGCCCCTCCACACCAGCCCGTTATAT 266

Qy  611 CTCTGCATCCATAGCAAGTAGCCTAATGTTTCTGTGTCTAGGTGTCATCTCTGTGAATCG 670
        |||  ||||   | | ||
Db  265 AGCTAGGGCTGGGTGAGATAATCT------------------------- 242

Qy  671 AGATCCTTGCCTTGCTTGCATTAGGGAGGCACAAAATACTCAGAGATTCAAGAGACTGCTC 730
        ------------------------------------------------------------
Db  241 ---------------------------------------- 242

Qy  731 AGCAGCCCAGAGTCTTCTCCTCAAAGGAAAGGTCTCAACTCTCAGCCCCCTTAGCTCTGA 790
        |||  | || ||
Db  241 ------TCCAGCCTGGGAAGCCAAGTCACACACCCCTGCCCCCACCAGTGCC--- 197

Qy  791 GTCAGGCCTGGAACAAACGCCACAGGAATGAGAAAAGCTGCCATAGTGCTCTTGTCACTT 850
        |  |||| |||
Db  196 --------AATTCAGAGCAGTGAATTTTCATTCCAGACTTAGTGTCTCGGGAAGCC 148

Qy  851 CAAGAGGTCAAAGAAAATAGTGTTAACCATGAAAAACGAGAAGACCAACAGTTATCCATTG 910
        ||||||| |||
Db  147 CAAGAGGAGGATGACAA- 131

Qy  911 ATAGCGTCTCAGGACAGATAGGACAGAGAGAACACTAGGAGAGGGGAACCCACGAAGGAC 970
        ------------------------------------------------------------
Db  130 ---------------------------------------- 131

Qy  971 AAGGTATTAGTAGTTGGTTTCAGGGCAATGTCTTGTACTGAAGATTCTAGAAAACACAA 1030
        -----------------------------------------------------------
Db  130 ---------------------------------------- 131

Qy 1031 TTTGCTGGTTGAACAGCTGAAGTGGGGTGGGGGGTTCTTACCCCATGTTCATGGAAGGGTG 1090
        ------------------------------------------------------------
Db  130 ---------------------------------------- 131

Qy 1091 AGTGAGGAGGAGACAGAGATATATGATGGCCAGCATAACAAACATACAACACCCTAATTAA 1150
        ------------------------------------------------------------
Db  130 ---------------------------------------- 131

Qy 1151 CACTTCCCTCTTCACTGACACCCCCTTCACTCTCTTCATAAAAAATAAAAAAAGT 1210
        ------------------------------------------------------
Db  130 ---------------------------------------- 131

Qy 1211 ATTTTATGTGGCTCTTACGATAGAATCTTTCCTGAACTATAAAAAGATCTAAATATTTA 1270
        ----------------------------------------------------------
Db  130 ---------------------------------------- 131

Qy 1271 TATTTTTCACATTTTAATATCTTAGCGATGACAAGCCAGAAACAAGTATTTTTTGCCTCT 1330
        -----------------------------------------------------------
Db  130 ---------------------------------------- 131

Qy 1331 CTCAACAGCAAAGCTTGGGGCCTTTTGTTTCCGTGTTAGGAATAGAACACGAGAGCCCCC 1390
        ||||  ||||
Db  130 --------------GCTGGCCGCGGCGGGTATGCGAATCAGCAGGAGA------- 101
```

Database :   new.seq.*

            Maximum Match 100%
            Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES

                      %
Result   Query
No.   Score   Match Length DB ID   Description
------ ------ ----- ------ -- -----   -----------
  1   202.2   58.4   337   1 QUERY_1   Entered [bobryen
c 2   15   4.3   337   1 QUERY_1   Entered [bobryen

                            ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   58.4%;   Score 202.2;   DB 1;   Length 337;
Best Local Similarity 80.8%;   Pred. No. 0;
Matches 277; Conservative 0; Mismatches 58; Indels 8; Gaps 4;

Qy   1 GCAATGTCAACAGACAGCTGTCCCCTGAC-TCTTGACAAATAGGATGACTTGCATTGCTG 59
           |||| |||| |||||||||||||||||| |||| | | | |||||| ||||||||||
Db   1 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG 60

Qy   60 AGGGATGTGATCACCACCAAAGGAATGGCCCCTCACATTTCTTCCTGATTCACATATTC 119
           || ||||| |||||||| |||||| |||| ||||||||| ||| |||||||||||||
Db   61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCCACATTTCTTCCTGATTCGCATACGC 120

Qy   120 AGCAGGGTTAGCTTGTCCTCCCCCCTTCAGCTTCCCAGACACAGCTGAGTCTGGAATGA 179
           || |||||| |||||||| ||||||||||||||| |||||||||||
Db   121 CGCGG-----CCAGCTTGTCATCTCCCTTGGGCTTCCCAGACACTAAGTCTGGAATGA 175

Qy   180 AAATTCACCTGCCTCGAGTTGGCCTCCTAATGGGGGGCGGGAGTGTTACTTCCGGTTCCCAG 239
           ||||||||||||||||||||| |||| |||||||||||||||| ||||||||||||||
Db   176 AAATTCACCTGCCTCGAGTTGGCCACTGGGTGGGGGGGCGGGAGTGTGACTTGGCTTCCCAG 235

Qy   240 GTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGGGGCCCAG 299
           |||||||||||||||||||| ||||| ||||||||| | ||||| ||||||||||| |||
Db   236 GCTGGAAGATTATCTCACCCAGCCCCTAGCTATATAA-CGGGCTGGTGTGGAGGGGCTCCA 294

Qy   300 CAGGGCCAACTCCAGGGATTCCTTC-CACGACAGAAAAACATA 341
           ||||||| |||||||||| |||||| | ||||||||||||||
Db   295 CAGGGCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   4.3%;   Score 15;   DB 1;   Length 337;
Best Local Similarity 26.7%;   Pred. No. 0;
Matches 62; Conservative 0; Mismatches 45; Indels 125; Gaps 2;

Qy   85 TGGCCCCTCACATTTCTTCCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCCCCCTC 144
          ||| |||| || || |||| || || |||
Db   294 TGGAGCCCCTCCACACCAGCCCGTTATATAGCTGGGCTGGTGTGGAGATAATCTTCC---- 239

Qy   145 CCTCTTCAGCTTCCCAGACACTGAGTCTGGAATGAAATGAAATTCACCTGCCTCGAGTTGGCT 204
          || |||||||| |||||||||| |||||
Db   238 ------------AGCCTGGGAAGCCAAGTCACACCCCT---------- 213

Qy   205 CCTAATGGGGGGCGGGAGTGTTACTTCCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCC 264

Qy 1391 GTGTATCTAGGCAGATGCTCTATCATTAGCCCATGAGTCTCCAGCGCCTCAGACGCACATTT 1450
Db   100 -- 101

Qy 1451 TTCTCGGGCTCTCTTAAGCTTTCCCACAGCATTGGGAAACTTTACTGACAGCATCCAAG 1510
Db   100 -- 101

Qy 1511 TTGTGCTTCTGCTAAGAACTGGACTCACATCTCTGTGCATCACTTCGGCCCGTTTTGG 1570
Db   100 -- 101

Qy 1571 GGTAGATCCTCGATTAGCCTTCAGATTTAGAACACGGTGAGCCTGTGTGCACTAATTA 1630
Db   100 -- 101

Qy 1631 TGGCCAGTGACACCCATAGAGTCAAAGTGCATTACTGAATGCTTTCAATTTCTCCTAATGC 1690
Db   100 -- 101

Qy 1691 TGGTACGATGGCATGTCACGGGCCATTTTAGTCTGCAGACATCACTCCAGAGAATTCCAA 1750
Db   100 ----------AATGTGAGAGGGTCATTCCTTTGGCAGTGACCACACC----------- 64

Qy 1751 ACAGATAGAGACAAGTGGCACCCAGACCCCATCTCCTTCCCCTCGGCGCTGATTATCCCCAG 1810
Db   64 -- 64

Qy 1811 AAATAGGATGTCCCAAAGCAACACTTCCCAGCCAACTGGAGTGCTGATAAGTCCAGTTAT 1870
Db   64 -- 64

Qy 1871 CAGAAAGATATGGCTGTAGTGTGATGCACAGTGCTTGCATTTTCTTGATACGTTAGTCA 1930
Db   64 -- 64

Qy 1931 TATGAGAGCTGACAAAGAGGAGGAAAAAGAGCCGATGTGTGCAATATTAACAGGCAGCT 1990
Db   64 -- 64

Qy 1991 GTCCCCTGGCTTCCGATACGTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCC 2049
            ||| ||| |||| ||||
Db   63 --GCTCAGCAATGCGAGTCATCCCACGTATCGGGAAGCCAGGGGACAGCTGCC 13

Search completed: May 25, 2005, 16:34:53
Job time : 1.87204 secs

            GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:34:51 ; Search time 0.127959 Seconds
                            (without alignments)
                            1.822 Million cell updates/sec

Title: US-10-005-337A-2_1715-2060
Perfect score: 346
Sequence: 1 gcaatgtcaacagacagctg.........cgacagaaaacatacaaga 346
Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.0
Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

```
Db       212 --------------------------------------------------------- 213

Qy       265 CAGCTATATAAGCTGACCGGTGTGGAGGGCCCAGCAGGGCCAACTCCAGGG 316
                        |||||||| ||| |||||| |||||
Db       212 ---------------GCCCCCACCAGTGGCCAATTCAGAG 188
```

Search completed: May 25, 2005, 16:34:53
Job time : 0.127959 secs

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          GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          May 25, 2005, 16:35:35 ; Search time 0.001 Seconds
                                          (without alignments)
                                          1589.292 Million cell updates/sec

Title:          US-10-005-337A-1-COPY
Perfect score:  2358
Sequence:       1 ggatcccttcatgtttaaca.........caggtcggaggcaccatgg 2358

Scoring table:  IDENTITY NUC
                Gapop 1.0 , Gapext 1.0

Searched:       1 seqs, 337 residues

Total number of hits satisfying chosen parameters:     2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      new.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

                           %
Result          Query
No.    Score   Match   Length  DB  ID        Description
-------------------------------------------------------------------
 1      337    14.3     337     1   QUERY_1   Entered [bobryen
 c  2   40.8    1.7     337     1   QUERY_1   Entered [bobryen

                                ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match            14.3%; Score 337; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1972 GCAATATTAAACAGGCAGCTGTCCCCTGGCTTCCGATACGTGGGATGACTCGCATTGCTG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAATATTAAACAGGCAGCTGTCCCCTGGCTTCCGATACGTGGGATGACTCGCATTGCTG 60

Qy   2032 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTCTTCCTGATTCGCATACGC 2091
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTCTTCCTGATTCGCATACGC 120

Qy   2092 CCGGGCCAGCTTGTCATCTCCCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 2151
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCGGCCAGCTTGTCATCTCCCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 180

Qy   2152 CACCTGCCTCTGAATTGGCCACTGGTGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGG 2211
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CACCTGCCTCTGAATTGGCCACTGGTGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGG 240

Qy   2212 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGTGGAGGGGCTCCACAGGGC 2271
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGTGGAGGGGCTCCACAGGGC 300

Qy   2272 CAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATA 2308
          |||||||||||||||||||||||||||||||||||||
Db    301 CAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match             1.7%; Score 40.8; DB 1; Length 337;
Best Local Similarity  53.8%; Pred. No. 0;
Matches 170; Conservative 0; Mismatches 107; Indels 39; Gaps 26;

Qy   2054 GAATGACCCTCTCACATTCTTCCTGATTCGCATACGCCGGGCCAGCTGTCATCTCCC 2113
          |||||  ||| || |||||   ||||||  ||| | |  ||| |||  |
Db    319 GGATGAACCCCT-GGAACTGGCCCTGTGGAGC-CCCTCCAC-ACCAGCCCGTTATAT--A 265

Qy   2114 TCTTGGGCT-TCCCAGACA--CT--AAGTCTGAATGAAAATTCA----CCTG-CCTCTG 2163
          ||  |||||    | | |   ||    ||| |||| | | |||        | ||| |
Db    264 GCTAGGGCTGGGTGAGATAATCTTCCAGCCTGGGAGCCAGTCACACCCTGCCCCCAC 205

Qy   2164 AATTGGCCACTGGTGGGGCCAGGGGTGTGACTTGGCTTCCCAGCCTGGAAGATTATCTCA 2223
          ||  ||||| |  |||| ||| | |    |  ||   | |||| |   ||| |   |
Db    204 CAGTGGCCAAT-TCAGAGGCAG---GTGAATTTTCATTCCAGACT--TAG--TGTCT-G 155

Qy   2224 CCCAGCCC--TAGCTATATAACGGCGTCGT-GTGGAGG-GGCTCCACAGGGCCA-GTTCC 2278
          |||  |||   || || | | || | ||   |||||||   ||   |  |   ||
Db    154 GGAAGCCCAAGAGAGGGAGATGACAAGCTGGCCGCGCGGCTGATGCGATGCAAGGAAAGAAATGTG 95

Qy   2279 AGGGGTTCATCCACAAGAGAG-AAAAACATAGACTCGAGGTCTAGGGAGCTTGCATGCCT 2337
          |||  |||||| |   |||||    ||||| ||    ||  | |||||  ||| | |||
Db     94 AGAGGGTCATTCCTTGGCAGTGACCACCG-CTC-AGCAAT-GCGAG--T-CAT-CCC 42

Qy   2338 GCAGGTC-GGAGGCCA 2352
          |||| || |||  |||
Db     41 ACGTATCCGGGAAGCCA 26

Search completed: May 25, 2005, 16:35:35
Job time : 0.001 secs

          GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          May 25, 2005, 16:35:35 ; Search time 0.001 Seconds
                                          (without alignments)
                                          233.204 Million cell updates/sec

Title:          US-10-005-337A-2_1715-2060
Perfect score:  346
Sequence:       1 gcaatgtcaacagacagctg.........cgacagaaaacatacaaga 346

Scoring table:  IDENTITY NUC
                Gapop 1.0 , Gapext 1.0

Searched:       1 seqs, 337 residues

Total number of hits satisfying chosen parameters:     2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
```

Database :   new.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES

         %
Result   Query
No.   Score Match Length DB ID   Description
---- ----- ----- ------ -- ------   -----------
  1 238.8   69.0   337 1 QUERY_1   Entered [bobryen
c 2   36.8   10.6   337 1 QUERY_1   Entered [bobryen

                        ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   69.0%; Score 238.8; DB 1; Length 337;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 283;   Conservative 0; Mismatches 52; Indels 8; Gaps 5;

Qy   1 GCAATGTCAACAGACAGCTGTCCCCTGAC-TCTTGACAAATAGGATGACTTGCATTGCTG 59
          |||||| ||| ||||| ||| |||||||| | | |||||| |||||| ||||||||
Db   1 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTTCGCATTGCTG 60

Qy   60 AGGGATGTGATCACCACCAAAAGAAATGGCCCTCTCACATTTCTTCCTGATTCACATATTC 119
          |||| || || ||| |||||||||||||| ||| ||||||| ||||||||||||||||
Db   61 AGCGGTGTGCTCACTGCCAAAAGGAATGACCCCTCTCACATTTCTTCCTGATTCGCATACGC 120

Qy 120 AGCAGGGTTAGCTTGCTGTCCTCCCCCTCCTCAGCTTCCCAGACACTGAGTCTGGAATGA 179
          ||||| |||| |||||||| |||| |||||||||| |||||||||||||||||||||
Db 121 CGC--GGCCAGCTTGTCAT---CTCCCCTCTGGGCTTCCCAGACACTAAGTCTGGAATGA 175

Qy 180 AAATTCACCTGCCCTCGAGTTGGCTCCTAATGGGGGCGGGAGTGTTACTTCGGTTCCCAG 239
          ||||||||||||||||||||||||| |||||||| |||||| |||||||||||||||||
Db 176 AAATTCACCTGCCCTCGAATTGGCCACTGGTGGGGCAGGGGTGTGACTTGGCTTCCCAG 235

Qy 240 GTTGGAAGATTATCTCACCCGCCCCAGCTATATAAGCTGACCCGGTGTGGAGGGGCCCAG 299
          ||||||||||||| |||||||||||||||||||| |||||| |||||||||||||||
Db 236 GCTGAAGAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTGCTGTGTGGAGGGGCTCCA 294

Qy 300 CAGGGCCAACTCCAGGGATTCCTTC-CACGACGAAAAACATA 341
          |||||||| ||||||||||||||| |||||||||||||||||
Db 295 CAGGGCCAGTTCCAGGGGTTCATCCACCACAAGAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   10.6%; Score 36.8; DB 1; Length 337;
Best Local Similarity 55.3%; Pred. No. 0;
Matches 146;   Conservative 0; Mismatches 82; Indels 36; Gaps 24;

Qy   42 GGATGA---CTTGCATTGCTGAGCGATGT-GATCACCACCAAAGGAATGGCCCTCTCACA 97
          ||||| | | ||| | | ||||| | ||||| ||||| |||| ||||| ||||
Db 319 GGATGAACCCCTGGAA--CTG-GCCCTGTGGAGCCCTCCACACCA---GCCC-GTTATA 267

Qy   98 TTTCT--TCCTGATTCACATA---TT-CAGCAGGGTTAG-CTTGTC-CTCCCCT-CCCTC 148
          |||| |||| |||||||| || |||||||| ||| |||| |||||| |||| |
Db 266 TAGCTAGGGCTGGGTGAGATAATCTTCCAGCCTGGGAAGCCAAGTCACACCCCCTGCCCCC 207

Qy 149 TTCAGCTTCCCAGACACTGAGTCTGGAATGAAAATTCA--CCTGCCTCTGAGT-TGG--C 203
          || ||| ||| ||| ||||| |||||| |||||| | | | || ||| || |
Db 206 ACCAG-TGGCCA-ATTCAGAGGCAGG--TGAATTTCATTCCAGACTTAGTGTCTGGGAA 151

```
              GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:        May 25, 2005, 16:36:21 ; Search time 0.872041 Seconds
                                        (without alignments)
                                        1.822 Million cell updates/sec

Title:          US-10-005-337A-1-COPY
Perfect score:  2358
Sequence:       1 ggatcctttcatgttaaca.........cagtcggaggccaccatgg 2358

Scoring table:  IDENTITY_NUC
                Gapop 0.5 , Gapext 0.0

Searched:       1 seqs, 337 residues

Total number of hits satisfying chosen parameters:    2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      new.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result            %    Query
No.    Score    Match  Length  DB  ID          Description
----   -----    -----  ------  --  --          -----------
  1     337     14.3    337    1   QUERY_1     Entered [bobryen
c 2     282.5   12.0    337    1   QUERY_1     Entered [bobryen

                              ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match      14.3%;  Score 337;  DB 1;  Length 337;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 337;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  1972 GCAATATTAACAGGACCAGCTGTCCCTGCTTCCCGATACGTGGGATGACTCGGATTGCTG 2031
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GCAATATTAACAGGACCAGCTGTCCCTGCTTCCCGATACGTGGGATGACTCGGATTGCTG 60

Qy  2032 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTTCTTCCTGATTCGCATACGC 2091
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTTCTTCCTGATTCGCATACGC 120

Qy  2092 CGCGGCCAGCTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 2151
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGCGGCCAGCTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 180

Qy  2152 CACCTGCCTCTGAATTGGCCACTGGTGGGGACAGCAGGGGTGTGACTTGGCTTCCCAGGCTGG 2211
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CACCTGCCTCTGAATTGGCCACTGGTGGGGACAGCAGGGGTGTGACTTGGCTTCCCAGGCTGG 240

Qy  2212 AAGATTATCTCACCCAGCCCTAGTATATAACCGGGCTGGTGTGGAGGGGCTCCACAGGGC 2271
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGATTATCTCACCCAGCCCTAGTATATAACCGGGCTGGTGTGGAGGGGCTCCACAGGGC 300

Qy  2272 CAGTTCCAGGGGTCATCCACAAGAGAGAAAAACATA 2308
         ||||||||||||||||||||||||||||||||||||
Db   301 CAGTTCCAGGGGTCATCCACAAGAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match      12.0%;  Score 282.5;  DB 1;  Length 337;
Best Local Similarity   14.6%;  Pred. No. 0;
Matches 337;  Conservative 0;  Mismatches 0;  Indels 1973;  Gaps 109;

Qy    22 TATCAACCCTAACCCAAGGGAACAGCCTGCCTCGACAGTCAGTGGCTTGCCACCCATGAATAC 81
         |||
Db   337 TAT--- 335

Qy    82 TTCCTAGTCCGTTGTGAAACTCAGCGCCATCCCAACACTTCTGCAAGCCCCATCC 141
                                              |||| 
Db   334 -----GTTT-                        TTCT 327

Qy   142 TCTACAAGGTGCTCATTGGGAAATTTCCTGGAGCTTCTCCTTCAGGATCAGCCTGATTCTA 201
         ||| |||              |||
Db   326 CTC-TTG              TGA 314

Qy   202 GGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGAATCAAACGACCCTTTAC 261
                                              ||||||
Db   313 ----------ACCCCT-----GGAA 304

Qy   262 AGGGGTCACATATCATCATCCTATATGTCAGGTATTACATTACGATTCGTAACAGTAG 321
                                                         
Db   303 ----CT 302

Qy   322 CAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCAACAT 381
         
Db   301 ------- 302

Qy   382 GAGGCCGCACACTGTTCTAGAGAAAAATCACCTGGGTGGGGAAAGGTTTGGGAAAGCCT 441
         |||| ||||                                        GG--AGCC-
Db   301 -GGCC-----CTGT- 288

Qy   442 TTCTGTCCATTCTTCATTCTTCAAAGTGATGTGTTCAGAGAAAGCCTTTCAGCTGTTCTG 501
                                        CACA----C----CAGC----C--
Db   287 ---CC----TC- 274

Qy   502 CTGGGGCTCTTAGTAGTCGTGAGTAGGAACTGTATGTACCAGGTCTGCTTCTTATGGGTG 561
         C----G--TTA-TA------TAG--CT------AGG--GC------TGGGTG
Db   273 C----G--TTA-TA------TAG--CT------AGG--GC 251

Qy   562 GAGCCAAGACGCATCGTGGTGGTGAGCGAAGACGCAACCTCACCTTCACGTCTGCATCCA 621
                                                          AA------TCT---TCC-
Db   250 -----AGA------T 239

Qy   622 TAGCAAGTAGCCTAATGTTTCTGTGTCATCTCTGTGGTGTCATCTCTGTGAATCGAGATCCTTGGC 681
                                                                  TGG-
Db   238 ------AGCC 232

Qy   682 CTTGCTTGAATTAGGGAGGCACAAAATACTCAGAGATTCAAGACTGCTCAGCAGCCCAGA 741
                                        CAAG----TCA-CA-CCC-
Db   231 ------GAA------GC 215

Qy   742 GTCCTTCCTCAAAGGAAAGTCTCAACTCTCAGCCCCCCTTAGCTCTGAGTCAGGCCTGG 801
                                        CT--GCCCCC
Db   214 ------------ 207

Qy   802 AACAAACGGCCACAGGAATGAGAAAAAGCTGCCATAGCTGCTTGTCACTTCAAGAGGTCAA 861
                                        GCCA------A-TTC-AGAG-C--
Db   206 -----AC-----CAG---TG 186
```

```
Qy   862 AGAAAAATAGTGTTAACCATGAAAACGAGAGACCAACAGTTATCCATTGATAGGGTCTCA 921
             ||  |||  | ||                         ||| ||||
Db   185 AG-----GTG--A-AT--------------------------TT-T-CATT-------- 171

Qy   922 GGACAGATAGGACAGAGAACTAGGAGAGGGAACCCACGAAGACAAGGTATTAGT 981
             |||| ||                         ||| |    |||||
Db   170 ----------CCA-----GAC------TTAGT 160

Qy   982 GTGTTGGTTTTCAGGGCAATGTCTTGTACTGAAGATTCTAGAAACACAATTTGCTGGTTG 1041
         || |||                         |||
Db   159 GT-----------------------------CTGG-- 154

Qy  1042 AACAGCTGAAGTGGGGTGGGGGTTCTTACCCCATGTTCATGGAAGGGTGAGTGAGGAGAG 1101
             ||||                         ||||
Db   153 -----GAAG-------------------CCCA------ 142

Qy  1102 ACAGATATATGATGGCCAGCAATACAAACATACCACACCCTAATTAACACTTCCCTCT 1161
                                         ||||
Db   142 ---------------------------------------------------------- 141

Qy  1162 TCTACTGACACCCCCTTCACTCTCCTCTTTCATAAAAAATAAAAAAAGTATTTTATGTGG 1221
                                                                ||
Db   141 --------------------------------------------------GG 140

Qy  1222 CTCTTACGATAGAATCTTTCCTGAACTATAAAAAGATCTAAATATTATATTTTCACA 1281
         ------------------------------------------------------------ 140

Qy  1282 TTTTAAATATCTTAGCGATGACAAGCCAGAAAACAAAGTATTTTTGCCTCTCTCAACAGCAA 1341
                ||||||||
Db   139 -----A--GATGACAAGC-------------------------------------- 129

Qy  1342 AGCTTGGGGCCTTTTGTTTCCGTGTTAGGAATAGAACAGAGAGCCCCGTGTATCTAGG 1401
                ||||                         || |
Db   128 ----TGG-----------CCG----------------------------CG--GC---GTAT-----G 114

Qy  1402 CAGATGCTCTATCATTAGCCCATGAGTCTCCAGCTCAGACGCACATTTTCTCGGGCTC 1461
             || ||                         |||
Db   113 C-GA----------ATCA----------------------------------------------- 107

Qy  1462 TCTTTAAGCTTTTCCCACAGCATTGGGAAACTTTACTGACAGCATCCAGTTGTGCTTCTG 1521
             ||||                         |||   |
Db   106 -----------------------------GGAA------GA------TGTG----- 95

Qy  1522 CTAAGAACTGGACTCACATCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGTAGATCCTC 1581
             |||                         |||    |
Db    94 ---AGA-------------------------------GGG------TC 87

Qy  1582 TGATTAGCCTTCAGATTTAGAACACGGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGAC 1641
              ||| ||||||
Db    86 --ATT--CCTT------------------------------TGG-CAGTGAC 70

Qy  1642 ACCATAGAGTCAAAGTGCATTACTGAAATGCTTTCAATTTCTCCTAATGCTGGTACGATGG 1701
         ---------------------------------------------------------- 70

Qy  1702 CTAAGAACTGCAGGGGCCATTTTAGCTCGACAACATCACTCCAGAGAATTCCAAACAGATAGAGA 1761
                                         |||
Db    69 -----------------------------------CAGC------ 66

Qy  1762 CAAGTGGCACCCAGACCCATCTCCTTCCCCTCGGGCTGATTATCCCGAGAAATAGGATGT 1821
                                         |||
Db    69 ---------------------------CC----GCT------ 61

Qy  1822 CCCAAAGCAACACTTCCCAGCCAACTGAGTGCTGATAAGTCCAGTTATCAGAAAGATAT 1881
                                         |||
Db    60 ----------------------------CAGC------ 57

Qy  1882 GGCTGTAAGTGTGATGCACAGTGCTTGCATTTTCTTGTCATTTGTTAGTCATATGAGAGCTG 1941
              ||  || |||||
Db    56 ------AA-------TG---CG--AGTCA------- 46

Qy  1942 ACAAAGAAGGAAAAAGAGCAGCGATGTGGTGCAATATTAACAGGCAGCTGTCCCCTGGCT 2001
```

```
Db    45 ---------------------------------------------------------- 46

Qy  2002 TCCCGATACGTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACC 2061
         |||| ||||                         || |
Db    45 TCCC--ACGT----------------AT-----CG-- 30

Qy  2062 CCTCACATTTCTTCCTGATTCGCATACGCCGCGGCCAGCTTGTCATCTCCCTTGGGC 2121
         ||                         ||||
Db    29 --------------------------GGG- 23

Qy  2122 TTCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGG 2181
         ||                         ||||
Db    22 ------GACA------ 19

Qy  2182 GCAGGGGTGTGACTTGGCTTCCCAGGCTGAAGAGATTATCTCACCCAGCTATATA 2241
                                         ||||
Db    18 ---------------------------GCTG------CCT-- 12

Qy  2242 ACGGGCTGGTGTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGTCATCCACAAGAGAGAA 2301
                                         |||
Db    11 --------------------------------------GTT-- 9

Qy  2302 AAACATAGACTCGGAGGTCTAGGGAGCTTGC 2331
         ||         || ||||
Db     8 -AA-------------------TA-------TTGC 1
```

Search completed: May 25, 2005, 16:36:23
Job time : 1.87204 secs

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OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:36:21 ; Search time 0.127959 Seconds
                    (without alignments)
                    1.822 Million cell updates/sec

Title: US-10-005-337A-2_1715-2060
Perfect score: 346
Sequence: 1 gcaatgtcaacagacagctg..........cgacagaaaacatacaaga 346

Scoring table: IDENTITY_NUC
                    Gapop 0.5 , Gapext 0.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   new.seq:*

                    Pred. No. is the number of results predicted by chance to have a
                    score greater than or equal to the score of the result being printed,
                    and is derived by analysis of the total score distribution.

                              SUMMARIES

                         %
Result   Query   Match   DB
No.   Score   Length   Match Length DB ID   Description
-----   -----   -----   ----- ----- ----- --   -----------
  1   262.5   75.9   337   1   QUERY_1   Entered [bobryen
c 2   159.6   46.1   337   1   QUERY_1   Entered [bobryen

```
Db  141 -GG-AGATGA---CAAGCTGCCGCGGGC----G--TAT--GC-GAATCAGGAAGAAATG  97
Qy  287 TG-GAGGGGC---CC--AGCAG-GGCCA-ACTC---CAG---G-GA-T--TCCTTCCA  326
        ||| |||||||      |||||||||| ||||     ||||    || | ||||||||
Db   96 TGAGAGGGGTCATTCCTTTGGCAGTGACCACAC-CGCTCAGCAATGCGAGTCATC---CCA  41
Qy  327 CG-A-CAGAAA---A---ACA-------TACA-A--G  345
        ||| | |||||   |    ||||        |||  |
Db   40 CGTATCGGGAAGCCAGGGACCAGCTGCCTGTTA-ATATTG  2
```

Search completed: May 25, 2005, 16:36:23
Job time : 0.127959 secs

ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   75.9%;   Score 262.5;   DB 1;   Length 337;
Best Local Similarity 79.9%;   Pred. No. 0;
Matches 290;   Conservative   0;   Mismatches 25;   Indels 48;   Gaps 25;

```
Qy    1 GCAATGTCAACAGACAGCTGTCCCCT-GACTCTT---GACAAATA---GGATGACTTGC   52
        |||| |||||||||||||||||||||| |||  |||    |||||    |||||||||||
Db    1 GCAATATTAACAGGCAGCTGTCCCCTGG---CTTCCCG----ATACGTGGGATGACTCGC   53

Qy   53 ATTGCTGAGCGATGTGATCAC--CACCAAAGGAATGGCCCTCTCACATTTCTTCCTGATT  110
        ||||||||||| |||| |||   |||||||||||| |||||||||||||||||||||||||
Db   54 ATTGCTGAGCGGTGTGGTCACTGC--CAAAGGAATGACCCTCTCACATTTCTTCCTGATT  111

Qy  111 CACATATTCAGCAG-GGTTAGCTTGTCCTCCCCCCTCCTTCAG--CTTCCCAGACACTG  167
        | ||||  ||| |||   ||||||||| ||     | ||||||     ||||||||||||
Db  112 CGCATA--C-GCCGGCGGCCAGCTTGTCAT---CTCCCTCTT-GGGCTTCCCAGACACTA  163

Qy  168 AGTCTGGAATGAAAATTCACCTGCCTCGAGTGGCTC-CTAATGGGGGC-GGGAGTGTT   225
        |||||||||||||||||||||||||||||| || | | ||  |||||| ||| |||| |
Db  164 AGTCTGGAATGAAAATTCACCTGCCTCGAATTGGC-CACTGGTGGGGGCAGGG-GTGTG  221

Qy  226 ACTTCGG-TTCCCAGGTTGGAAGATTATCTCACCGGCCCCAGCTATATAA---GCTGAC  281
        ||||  || ||||||| |||||||||||||||||||||| |||||||||      |||||
Db  222 ACTT--GGCTTCCCAGGCTGGAAGATTATCTCACCGGCCCTAGCTATATAACCGGGGCT---  277

Qy  282 CGGTGTCTGGAGGGGC-CCAGCAGGGCCAACTCCAGGGATTCCTTCCAC--GACAGAAAAAC  338
        |||||| |||||||| | |||||||||   ||||||| || || ||||    |||| |||||
Db  278 -GGTGTGGAGGGGTCCA-CAGGGCCCAGTTCCAGGGGTT-CATCCACAAGAGAGAAAAAC   334

Qy  339 ATA  341
        |||
Db  335 ATA  337
```

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   46.1%;   Score 159.6;   DB 1;   Length 337;
Best Local Similarity 45.2%;   Pred. No. 0;
Matches 208;   Conservative   0;   Mismatches   9;   Indels 243;   Gaps 86;

```
Qy    4 ATG--TCAACAGACAGCTGTCCCCTGACTCTTGACAAATAGGATGA--CTTGCATTGCTG   59
        |||     |         ||     || |  ||      ||||||    |    | |||||
Db  336 ATGTTT-----------T-T---CT-CTCTTG-----T-GGATGAACC---C----CTG  307

Qy   60 AGCGA--TG----TGATCACCACCAAAGGAATGGCCCTCT-CACATTTCTTCCTGA----  108
        | | |  ||       |    |    ||    |  |||  | ||      ||    |
Db  306 ---GAACTGGCCCTG-T---------GGA---GCCC-CTCCACA------CC--AGCCC  273

Qy  109 -TTCACATATTCAGC-AGGGTTAGCT---TGTCCTCCCCCTCCTTCAG---CTTCC   158
        |    |||  |||      ||||     ||                |    |||||
Db  272 GTT---ATAT--AGCTAGG----GCTGGGTG------AGATAATCTT-C   240

Qy  159 CAGACACTGAGTCTGGAATG--AA--AATTCA--CCTGC-----CTCTGAGTTGGCTCC  206
        ||| | ||     |||| |  |    |   |   | |          || ||  | |||
Db  239 CAG-C-CTG-----GGAA-GCCAAGTCA---CACCCCTGCCCCCAC-C--AG-TGG--CC  197

Qy  207 TAAT--G-GGGGC-GG-GAGTGTT--------ACTTCG-GT-T------CCC-AG-GT  241
        ||||   |   || || |   |          |  | || ||        ||| || ||
Db  196 -AATTCAGAG--GCAGGTGAAT-TTTCATTCCAGACTTAGTGTCTGGGAAGCCCAAGAG-  142

Qy  242 TGGAAGATTATCTCA------CC-CGGCCCCAGCTATATAAGCTGA--CCGG------TG  286
        ||||| |  |    |      || |             |   |  |   |||      ||
```

Left column

```
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OM nucleic - nucleic search, using sw model

Run on:        May 25, 2005, 16:37:10 ; Search time 0.872041 Seconds
                                      (without alignments)
                                      1.822 Million cell updates/sec

Title:          US-10-005-337A-1-COPY
Perfect score:  2358
Sequence:       1 ggatccttcatgtttaaca.........caggtcggaggcgaccatgg 2358

Scoring table:  IDENTITY_NUC
                Gapop 20_0 , Gapext 0.0

Searched:       1 seqs, 337 residues

Total number of hits satisfying chosen parameters:     2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      new.seq:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES

                     %
Result        Query
No.    Score  Match  Length DB ID            Description
-----  -----  -----  ------ -- -------        -----------
   1     337   14.3    337   1  QUERY_1        Entered [bobryen
 c 2    17.4    0.7    337   1  QUERY_1        Entered [bobryen

                             ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match     14.3%;  Score 337; DB 1; Length 337;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 337; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 1972 GCAATATTAACAGGCAGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG 2031
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GCAATATTAACAGGCAGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG 60

Qy 2032 AGCGGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTTCTTCCTGATTCGCATACGC 2091
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGCGGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTTCTTCCTGATTCGCATACGC 120

Qy 2092 CGCGGCCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 2151
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CGCGGCCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 180

Qy 2152 CACCTGCCTCTGAATTGGCCACTGGTGGGGACGCAGGGGGTGTGACTTGGCTTCCCAGGCTGG 2211
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CACCTGCCTCTGAATTGGCCACTGGTGGGGACGCAGGGGGTGTGACTTGGCTTCCCAGGCTGG 240

Qy 2212 AAGATTATCTCACCCAGCCCTAGCTATATAAACGGGCTGGTGTGGAGGGGGCTCCACAGGGC 2271
```

Right column

```
Db  241 AAGATTATCTCACCCAGCCCTAGCTATATAAACGGGCTGGTGTGGAGGGGGCTCCACAGGGC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2272 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 2308
        |||||||||||||||||||||||||||||||||||
Db  301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match       0.7%;  Score 17.4; DB 1; Length 337;
Best Local Similarity   53.7%; Pred. No. 0;
Matches 36; Conservative   0; Mismatches  31; Indels   0; Gaps   0;

Qy 1709 CAGGGCCATTTAGCTGCAGACATCACTCCAGAGAATTCAAACAGATAGAGACAAGTGG 1768
        ||||  |||||  ||||    |||| |  ||| ||||     |||||   ||||||
Db  186 CAGGTGAATTTCATTCCAGACTTAGTGTCTGGGAAGCCCAAGAGAGGGAGATGACAAGCTG 127

Qy 1769 CACCCAG 1775
        |   |||
Db  126 GCCGCGG 120

Search completed: May 25, 2005, 16:37:11
Job time : 0.872041 secs

                    GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        May 25, 2005, 16:37:10 ; Search time 0.127959 Seconds
                                      (without alignments)
                                      1.822 Million cell updates/sec

Title:          US-10-005-337A-2_1715-2060
Perfect score:  346
Sequence:       1 gcaatgtcaacagacagctg.........cgacagaaaacatacaaga 346

Scoring table:  IDENTITY_NUC
                Gapop 20_0 , Gapext 0.0

Searched:       1 seqs, 337 residues

Total number of hits satisfying chosen parameters:     2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      new.seq:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES

                     %
Result        Query
No.    Score  Match  Length DB ID            Description
-----  -----  -----  ------ -- -------        -----------
   1   169.6   49.0    337   1  QUERY_1        Entered [bobryen
 c 2    12.8    3.7    337   1  QUERY_1        Entered [bobryen

                             ALIGNMENTS
```

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   49.0%;   Score 169.6;   DB 1;   Length 337;
Best Local Similarity   75.1%;   Pred. No. 0;
Matches 257;   Conservative   0;   Mismatches   79;   Indels   6;   Gaps   2;

Qy   1 GCAATGTCAACAGACAGCTGTCCCCTGAC-TCTTGACAAATAGGATGACTTGCATTGCTG 59
        |||| |||| | |||||||||||||||||| | |||| || | | |||||| ||||||||
Db   1 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG 60

Qy   60 AGGCATGTGATCACCACCAAAGGAATGGCCCTCTCACATTCTTCCTGATTCACACATATTC 119
        |||| |||| |||| |||||||||||||||||||||||||||||||| |||| | |||
Db   61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCTCACATTTCTTCCTGATTCGCATACGC 120

Qy 120 AGCAGGGTTAGCTTGTCCTCCCCCTCCCTTCAGCTTCCCAGACACTGAGTCTGGAATGA 179
        ||| | ||||| ||| |||||||||||||||| ||||| |||||||||||
Db 121 CGCGG-----CCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGA 175

Qy 180 AAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGCCGGAGTGTTACTTCGGTTCCCAG 239
        ||||||||||||||||||| |||| ||| || ||||||||| ||| |||| | |||||
Db 176 AAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTCCCAG 235

Qy 240 GTTGGAAGATTATCTCACCGGCCCCAGTATATAAGCTGACCGGTGTGGAGGGGCCCAG 299
        | |||||||||||||||||||| |||| |||||||||| || ||| ||| |||||
Db 236 GCTGGAAGATTATCTCACCCAGCCCCTAGCTATATAACGGGCTCGTGTGGAGGGGCTCCAC 295

Qy 300 CAGGGCCAACTCCAGGGATTCCTTCCACGACACAGAAAAACATA 341
        ||||| ||||||||||||||||||||||||||||||||||||||
Db 296 AGGGCCCAGTTCCAGGGGGTTCATCCACAGAGAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   3.7%;   Score 12.8;   DB 1;   Length 337;
Best Local Similarity   51.8%;   Pred. No. 0;
Matches   29;   Conservative   0;   Mismatches   27;   Indels   0;   Gaps   0;

Qy   85 TGGCCCTCCACATTTCTTCCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCC 140
        ||| ||| | || | | | | | ||| ||| ||| || | || ||| ||
Db 294 TGGAGCCCCTCCACACCAGCCCGTTATATAGCTAGGGGCTGGGTCAGATAATCTTCC 239

Search completed: May 25, 2005, 16:37:11
Job time : 0.127959 secs

```
                GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        May 25, 2005, 16:37:50 ; Search time 0.001 Seconds
                                        (without alignments)
                                1589.292 Million cell updates/sec

Title:          US-10-005-337A-1-COPY
Perfect score:  2358
Sequence:       1 ggatcccttcatgtttaaca.........caggtcggaggccaccatgg 2358

Scoring table:  IDENTITY_NUC
                Gapop 60.0 , Gapext 0.0

Searched:       1 seqs, 337 residues

Total number of hits satisfying chosen parameters:     2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      new.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                        SUMMARIES

                %
Result          Query
No.     Score   Match Length DB ID       Description
----------------------------------------------------------
  1      337    14.3   337   1 QUERY_1   Entered [bobryen
c 2      17.4    0.7   337   1 QUERY_1   Entered [bobryen

                        ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match            14.3%;  Score 337; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 337;  Conservative  0; Mismatches 0; Indels 0;  Gaps  0;

Qy 1972 GCAATATTAACACGGCAGCTGTCCCCTGCTTCCCGATACGTGGGATGACTCGGCATTGCTG 2031
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GCAATATTAACACGGCAGCTGTCCCCTGCTTCCCGATACGTGGGATGACTCGGCATTGCTG 60

Qy 2032 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTTCTTCCTGATTCGCCATACGC 2091
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCACATTTCTTCCTGATTCGCCATACGC 120

Qy 2092 CGCGGCCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 2151
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CGCGGCCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 180

Qy 2152 CACCTGCCTCTGAATTGGCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGG 2211
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CACCTGCCTCTGAATTGGCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGG 240

Qy 2212 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGTGTGTGGAGGGGGCTCCACAGGGC 2271
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGTGTGTGGAGGGGGCTCCACAGGGC 300

Qy 2272 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 2308
        |||||||||||||||||||||||||||||||||||
Db  301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match             0.7%;  Score 17.4; DB 1; Length 337;
Best Local Similarity  53.7%; Pred. No. 0;
Matches 36;  Conservative  0; Mismatches 31; Indels 0;  Gaps  0;

Qy 1709 CAGGGCCATTTAGTCGACAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGG 1768
        |||| ||| ||| ||||||| | ||||  |    ||||  |||||| |  || |||| ||
Db  186 CAGGTGAATTTTCATTCCAGACTTAGTGTCTGGAAGCCCAAGAGGGGAGATGACAAGCTG 127

Qy 1769 CACCCAG 1775
        ||||| |
Db  126 GCCGCGG 120

Search completed: May 25, 2005, 16:37:51
Job time : 1 secs

                GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        May 25, 2005, 16:37:50 ; Search time 0.001 Seconds
                                        (without alignments)
                                233.204 Million cell updates/sec

Title:          US-10-005-337A-2_1715-2060
Perfect score:  346
Sequence:       1 gcaatgtcaacagacagctg.........cgacagaaaacatacaaga 346

Scoring table:  IDENTITY_NUC
                Gapop 60.0 , Gapext 0.0

Searched:       1 seqs, 337 residues

Total number of hits satisfying chosen parameters:     2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      new.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                        SUMMARIES

                %
Result          Query
No.     Score   Match Length DB ID       Description
----------------------------------------------------------
  1     128.6   37.2   337   1 QUERY_1   Entered [bobryen
c 2      12.8    3.7   337   1 QUERY_1   Entered [bobryen

                        ALIGNMENTS
```

```
RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match                37.2%;    Score 128.6;   DB 1;  Length 337;
Best Local Similarity      73.8%;    Pred. No. 0;
Matches  236;  Conservative  0;  Mismatches   79;  Indels    5;  Gaps    1;

Qy    22  CCCCTGACTCTTGACAAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAG   81
          ||||||  || ||| | ||  |   |||||||||||||||| |||| |||| |||||||
Db    23  CCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTGAGCGGTGTGTCACTGCCAAAG   82

Qy    82  GAATGGCCCTCTCACATTTCTTCCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCCC  141
          ||||||||||||||||||||||||||||||||   |||                  |
Db    83  GAATGACCCCTCTCACATTTCTTCCTGATTCGCATACGCCGCGGC-----CAGCTTGTCAT  137

Qy   142  CTCCCTCTTCAGCTTCCCAGACACTGAGTCTGGAATGAAAATTCACCTGCCTCTGAGTTG  201
          ||||||||||  |||||||||  || ||||||||||||||||||||||||||||  |||
Db   138  CTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAATGAAAATTCACCTGCCTCTGAATTG  197

Qy   202  GCTCCTAATGGGGGCGGGAGTGTTACTTCGGTTCGGTTCCCAGGTTGGAAGATTATCTCACCCG  261
          ||  | |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   198  GCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAG  257

Qy   262  CCCAGCTATATAAGCTGACCGGTGTGGAGGGGCCCAGCAGGGCCAACTCCAGGGATTCC  321
          ||||||||||||||||    || |||   |||       ||||
Db   258  CCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGGTTCAT  317

Qy   322  TTCCACGACAGAAAAACATA  341
          ||| ||||||||||||||
Db   318  CCACAAGAGAGAAAACATA  337


RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match                 3.7%;    Score 12.8;    DB 1;  Length 337;
Best Local Similarity      51.8%;    Pred. No. 0;
Matches   29;  Conservative  0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy    85  TGGCCCTCTCACATTTCTTCCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCC  140
          |||  ||   |  ||||  ||  || |  |       |  ||| ||| |  | ||
Db   294  TGGAGCCCCTCCACCAGCCCGTTATATAGCTAGGGCTGGGTCGAGATAATCTTCC  239
```

Search completed: May 25, 2005, 16:37:51
Job time : 0.001 secs

Copyright   GenCore version 5.1.6
             (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:38:25 ; Search time 0.872041 Seconds
                                           (without alignments)
                                           1.822 Million cell updates/sec

Title: US-10-005-337A-1-COPY
Perfect score: 2358
Sequence: 1 ggatccttcatgttaaca.........caggtcggaggccaccatgg 2358

Scoring table: IDENTITY_NUC
                   Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   new.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

                %
Result   Query
No.   Score   Match Length DB ID   Description
----   -----   ----- ------ -- --   -----------
  1   337   14.3   337   1 QUERY_1   Entered [bobryen
c 2   17.4   0.7   337   1 QUERY_1   Entered [bobryen

                                ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   14.3%;   Score 337; DB 1; Length 337;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 337; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1972 GCAATAATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCAATAATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG   60

Qy   2032 AGCGGTGTGGTCACTGCCAAAGGAATGACCCTCACATTTCTTCCTGATTCGCATACGC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCTCACATTTCTTCCTGATTCGCATACGC 120

Qy   2092 CGGGGCCAGCTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGCGGCCAGCTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 180

Qy   2152 CACCTGCCTCTGAATTGGCCACTGGTGGGGCAGGGGTGACTGGCTTCCCAGGCTGG 2211
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CACCTGCCTCTGAATTGGCCACTGGTGGGGCAGGGGTGACTGGCTTCCCAGGCTGG 240

Qy   2212 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC 2271

Db   241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2272 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 2308
          |||||||||||||||||||||||||||||||||||
Db   301 CAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match   0.7%;   Score 17.4; DB 1; Length 337;
Best Local Similarity   53.7%; Pred. No. 0;
Matches 36; Conservative   0; Mismatches   31; Indels   0; Gaps   0;

Qy   1709 CAGGGCCATTTAGTCGACACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGG 1768
          |||| |||||| |||||| | |||| ||||| |||||||
Db   186 CAGGTGAATTTCATTCCAGACTTAGTGTCTGGGAAGCCCAAGAGGGGAGGATGACAAGCTG 127

Qy   1769 CACCCAG 1775
          | |||
Db   126 GCCGCGG 120

Search completed: May 25, 2005, 16:38:26
Job time : 0.872041 secs

                   GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2005, 16:38:25 ; Search time 0.127959 Seconds
                                           (without alignments)
                                           1.822 Million cell updates/sec

Title: US-10-005-337A-2_1715-2060
Perfect score: 346
Sequence: 1 gcaatgtcaacagacagctg.........cgacagaaaacatacaaga 346

Scoring table: IDENTITY_NUC
                   Gapop 60.0 , Gapext 60.0

Searched: 1 seqs, 337 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   new.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

                %
Result   Query
No.   Score   Match Length DB ID   Description
----   -----   ----- ------ -- --   -----------
  1   120.8   34.9   337   1 QUERY_1   Entered [bobryen
c 2   12.8   3.7   337   1 QUERY_1   Entered [bobryen

                                ALIGNMENTS

```
RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match         34.9%;    Score 120.8;   DB 1;  Length 337;
Best Local Similarity   74.5%;         Pred. No. 0;
Matches  152; Conservative    0; Mismatches   52; Indels    0; Gaps    0;

Qy   138 TCCCTCCCTCTTCAGCTTCCCAGACACTGAGTCTGGAATGAAAATTCACCTGCCTCTGA 197
         || ||||||||||||||||||||||||   |||||||||||||||||||||||||||||
Db   134 TCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGA 193

Qy   198 GTTGGCTTCCTAATGGGGCGGGAGTGTTACTTCCGTTCCCAGGTTGGAAGATTATCTCAC 257
         |||||  ||  ||||||| || |||| ||  |  |||| |||||||||||||||||||||
Db   194 ATTGGCCACTGGTCGGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCAC 253

Qy   258 CCGCCCCAGCTATATAAGCTGACCGGTGTGGACGGGCCCAGCAGGGCCAACTCCAGGGA 317
         ||  |||||||   |||||    || |||       |||   |||    |||
Db   254 CCAGCCCTAGCTATATAACGGGGCTGGTGTGGAGGGGCTCCACAGGGCCCAGTTCCAGGGGT 313

Qy   318 TTCCTTCCACGACAGAAAAACATA 341
         ||  || ||||||||||||||||
Db   314 TCATCCACAAGAGAGAAAAACATA 337


RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match          3.7%;    Score 12.8;   DB 1;  Length 337;
Best Local Similarity   51.8%;         Pred. No. 0;
Matches   29; Conservative    0; Mismatches   27; Indels    0; Gaps    0;

Qy    85 TGGCCCTCTCACATTTCTTCCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCC 140
         |||   |||    |  |      |   |  |       || ||||  ||||||
Db   294 TGGAGCCCCTCCACACCAGCCCGTTATATAGCTAGGGCTGGGTGAGATAATCTTCC 239
```

Search completed: May 25, 2005, 16:38:26
Job time : 0.127959 secs

```
                GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       May 25, 2005, 16:39:04 ; Search time 0.001 Seconds
                                      (without alignments)
                                      1589.292 Million cell updates/sec

Title:        US-10-005-337A-1-COPY
Perfect score: 2358
Sequence:      1 ggatcccttcatgtttaaca.........caggtcggaggccaccatgg 2358

Scoring table: IDENTITY_NUC
               Gapop 0.5 , Gapext 60.0

Searched:      1 seqs, 337 residues

Total number of hits satisfying chosen parameters:   2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     new.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES

            %
Result          Query
No.   Score   Match  Length DB  ID         Description
1    337    14.3   337   1  QUERY_1    Entered [bobryen
c  2    17.4    0.7   337   1  QUERY_1    Entered [bobryen

                             ALIGNMENTS

RESULT 1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match           14.3%;  Score 337;  DB 1;  Length 337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches  337; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy  1972 GCAATATTAACAGGCAGCTGTCCCGATAACGTGGGATGACTCGCATTGCTG 2031
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GCAATATTAACAGGCAGCTGTCCCGATAACGTGGGATGACTCGCATTGCTG 60

Qy  2032 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCCACATTTCTTCCTGATTCGCATACGC 2091
         ||||||||||||||||||||||||||||||||||||||||||||
Db    61 AGCGGTGTGGTCACTGCCAAAGGAATGACCCCTCCACATTTCTTCCTGATTCGCATACGC 120

Qy  2092 CGCGGCCAGCTTGTCATCTCCCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 2151
         ||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGCGGCCAGCTTGTCATCTCCCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATT 180

Qy  2152 CACCTGCCTCTGAATTGGCCACTGGTGGGGCAGGGGTGACTTGGCTTCCCAGGCTGG 2211
         ||||||||||||||||||||||||||||||||||||||||||||
Db   181 CACCTGCCTCTGAATTGGCCACTGGTGGGGCAGGGGTGACTTGGCTTCCCAGGCTGG 240

Qy  2212 AAGATTATCTCACCCAGCCCTAGCTATATAAACGGGCTGGTGTGGACGGGGCTCCACAGGGC 2271

Db   241 AAGATTATCTCACCCAGCCCTAGCTATATAAACGGGCTGGTGTGGACGGGGCTCCACAGGGC 300

Qy  2272 CAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATA 2308
         |||||||||||||||||||||||||||||||||||||
Db   301 CAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATA 337

RESULT 2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match            0.7%;  Score 17.4;  DB 1;  Length 337;
Best Local Similarity 53.7%;  Pred. No. 0;
Matches   36; Conservative   0; Mismatches  31; Indels   0; Gaps   0;

Qy  1709 CAGGGCCATTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGG 1768
         |||| ||||| |||| ||| || ||||| |||  ||  |||||||  |||||||
Db   186 CAGGTGAATTTCATTCCAGACTTAGTGTCTGGAAGCCCAAGAGGGAGGATGACAAGCTG 127

Qy  1769 CACCCAG 1775
         |||||
Db   126 GCCGCGG 120

Search completed: May 25, 2005, 16:39:05
Job time : 1 secs

                GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       May 25, 2005, 16:39:04 ; Search time 0.001 Seconds
                                      (without alignments)
                                      233.204 Million cell updates/sec

Title:        US-10-005-337A-2_1715-2060
Perfect score: 346
Sequence:      1 gcaatgtcaacagacagctg.........cgacagaaaacatacaaga 346

Scoring table: IDENTITY_NUC
               Gapop 0.5 , Gapext 60.0

Searched:      1 seqs, 337 residues

Total number of hits satisfying chosen parameters:   2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     new.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES

            %
Result          Query
No.   Score   Match  Length DB  ID         Description
1    120.8   34.9   337   1  QUERY_1    Entered [bobryen
c  2    12.8    3.7   337   1  QUERY_1    Entered [bobryen

                             ALIGNMENTS
```

```
RESULT_1
QUERY_1
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match          34.9%;   Score 120.8;   DB 1;   Length 337;
Best Local Similarity   74.5%;   Pred. No. 0;
Matches  152;   Conservative   0;   Mismatches   52;   Indels   0;   Gaps   0;

Qy    138 TCCCTCCCTCTTCAGCTTCCCAGACACTGAGTCTGGAATGAAAATTCACCTGCCTCTGA 197
          || ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    134 TCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGA 193

Qy    198 GTTGGCTCCTAATGGGCGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCAC 257
          ||||| ||||||||||||| || ||||| |||||||||||||||||||||||||||||
Db    194 ATTGGCCACTGGTGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCAC 253

Qy    258 CCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGGGGCCCAGCAGGGCCAACTCCAGGGA 317
          ||||||||||||||||| | ||||||||||||||||||| ||| |||
Db    254 CCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGT 313

Qy    318 TTCCTTCCACGACAGAAAAACATA 341
          ||||||||  || || |||||||||
Db    314 TCATCCACAGAGAGAAAAACATA 337

RESULT_2
QUERY_1/c
; Entered [bobryen 25-May-05 16:13]
QUERY_1

Query Match           3.7%;   Score 12.8;   DB 1;   Length 337;
Best Local Similarity   51.8%;   Pred. No. 0;
Matches   29;   Conservative   0;   Mismatches   27;   Indels   0;   Gaps   0;

Qy     85 TGGCCCTCTCACATTTCTTCCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCC 140
          ||| || | ||----|--|||| || |
Db    294 TGGAGCCCCTCCACACCAGCCCGTTATATAGCTAGGGCTGGGTGAGATAATCTTCC 239

Search completed: May 25, 2005, 16:39:05
Job time : 0.001 secs
```